AMENDMENT — VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification

The paragraph at page 19, beginning at line 16 has been amended as follows:

PCR amplification of a pig MC4R gene fragment. Primers were designed from homologous regions of human and rat MC4R sequences (GenBank accession no. s77415 and u67863, respectively). The primers were: forward primer: 5'-TGG CAA TAG CCA AGA ACA AG-3' [(SEQ ID NO:6)] (SEQ. ID NO:5) and reverse primer: 5'-CAG GGG ATA GCA ACA GAT GA-3' [(SEQ ID NO:7)] (SEQ. ID NO:6). The PCR reaction was performed using 12.5 ng of porcine genomic DNA, 1x PCR buffer, 1.5 mM $MgCl_2$, 0.125 mM dNTPs, 0.3 mM of each primer, and 0.35 U *Taq* DNA polymerase (Promega) in a 10μL final volume. The conditions for PCR were as follows: 2 min at 94°C; 35 cycles of 30 s at 94°C, 1 min at 56°C, 1 min 30 s at 92°C, and a final 15 min extension at 72°C in a Robocycler (Stratagene, La Jolla, CA).

In the Claims

Please cancel claims 13-19 and 24-27.

Claims 1, 2, 4-6, 10, 12, 20, 23, 28, 29, 31, 32 have been amended as follows:

1. (Amended)

A method of identifying an animal which possesses a genotype [indicative of the] having a genetic marker associated with variation in metabolic traits [of] such as fat content, growth rate, and feed consumption, the method comprising:

a) obtaining a nucleic acid sample from the animal; and

b) identifying a [polymorphism] genotype characterized by a polymorphism in the seventh transmembrane domain in the MC4R [gene of the sample] protein wherein, said genotype is associated with variation in metabolic traits such as fat content, growth rate, and feed consumption.

2. (Amended)

The method of claim 1 wherein the polymorphism is characterized by a [nucleotide position 678 of the PCR product of the MC4R gene] site specific mutation at amino acid position 298 in the seventh transmembrane domain of the MC4R protein in pigs and any other animal.

4. (Amended)

The method of claim 2 wherein the polymorphism at [the nucleotide] amino acid position [678] 298 is associated with variation in fat content.

5. (Amended)

The method of claim 2 wherein [a guanine at the nucleotide position 678 is associated with lower feed intake] marker for lower feed intake than animals without marker, is identifiable by a mutation that replaces aspartic acid codon with asparagine codon at amino acid position 298 of MC4R protein.

6. (Amended)

The method of claim 2 wherein [an adenine at the nucleotide position 678 is associated with a faster rate of gain] marker for faster rate of gain, than animals without marker, is identifiable by a mutation that replaces aspartic acid codon with asparagine codon at amino acid position 298 of the MC4R protein.

10. (Amended)

The method of claim 1 further comprising the step of amplifying polymorphism in the MC4R gene sequence with allele specific oligonucleotide primers.

12. (Amended)

The amplified gene sequence of claim 10 wherein primers used in the amplification are selected from the group consisting of SEQ ID NO: 5, SEQ. ID NO:6, SEQ. ID NO:7, SEQ. ID NO:8, SEQ. ID NO:9, and SEQ. ID NO:10[, and SEQ. ID NO:11].

20. (Amended)

A method of identifying an animal which possess a desired genotype [indicative of the] having a genetic marker associated with metabolic traits of fat content, growth rate, and feed consumption, the method comprising:

a) obtaining a nucleic acid sample [of genomic DNA,] from an animal,

b) [digesting the sample with *Taq I* to obtain fragments,] amplifying nucleic acid of said sample with primers SEQ ID NO: 5 AND SEQ ID NO: 6,

[b] c) digesting the sample with T*aq I* to obtain fragments,

[c] d) separating the fragments obtained from the digestion, and

[d] e) identifying the presence or absence of a *Taq I* site [at base 678 of the PCR product of the MC4R gene] in an MC4R gene fragment to specify polymorphic site.

23. (Amended)

The method of claim 20 wherein the step of identifying comprises detecting the *Taq I* [site by amplification] restriction pattern.

28. (Amended)

A method for selecting animals for [the] a desired polymorphic traits indicative of lower fat content, faster growth rate, or lower feed consumption, than animals without said traits,

comprising [the steps of]:

a) obtaining a nucleic acid sample from an animal,

b) [identifying a polymorphism characterized by a nucleotide position 678 of a PCR product of the MC4R gene, and] amplifying the nucleic acid of said sample,

e) [b] c) identifying a polymorphism characterized [by a nucleotide position 678 of a PCR product of the MC4R gene] within a *Taq I* restriction recognition site, and

[c] d) selecting the animals which have [the] a nucleotide [associated with the desired traits in position 678] substitution of guanine to adenine within the *Taq I* restriction site within the MC4R gene.

29. (Amended)

A method for an indirect selection for a polymorphism in MC4R wherein specific alleles of an alternative DNA marker are used to make the indirect selection wherein the alternative DNA marker is a linked marker near MC4R comprising utilizing genetic linkage mapping techniques.

31. (Amended)

A method of identifying animals which possess a desired genotype having a genetic marker [indicative of the] associated with metabolic traits [of] such as fat content, growth rate, and feed consumption to determining the association between a MC4R genotype and a trait of interest, the method comprising:

a) [determining an association between a MC4R genotype and a trait of interest by] obtaining a sample of animals from a line or breed of interest,

b) preparing genomic DNA from each animal in the sample,

c) determining the genotype of the MC4R gene, and

d) calculating the association between the MC4R genotype and the trait.

32. (Amended)

A method of selecting animals which possess a desired MC4R genotype <u>having a genetic marker</u> [indicative of the] <u>associated with</u> metabolic traits [of] <u>such as</u> fat content, growth rate, and feed consumption, the method comprising:

a) obtaining a nucleic acid sample from an animal,

b) identifying the genotype of the MC4R gene of the animal, and

c) selecting those animals which have the genotype associated with the desired traits.

Please add new claim 33.

33. (New)

A method of identifying an animal which possess a desired polymorphism within the melanocortin-4 receptor protein of the seventh transmembrane domain comprising:

c) obtaining a nucleic acid sample from an animal;

d) identifying polymorphism by a nucleotide substitution within a *Taq I* site specific restriction pattern of the MC4R gene.